

#5

SEQUENCE LISTING

<110> Kao, Hung-Teh
Hartig, Paul R.
Branchek, Theresa

<120> DNA Encoding A Human Serotonin (5-HT2) Receptor and
Uses Thereof

<130> 35997a3zy/JPW

<140> 09/145,864

<141> 1998-09-02

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<170> PatentIn Ver. 2.1

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Ser	Leu	Met	Gln	Leu	Asn	Asp	Asp	Thr	Arg	Leu	Tyr	Ser	Asn	Asp	Phe	
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Asn	Ser	Gly	Glu	Ala	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Trp	Thr	Val	Asp	
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tct	gaa	aat	cga	acc	aac	ctt	tcc	tgt	gaa	ggg	tgc	ctc	tca	ccg	tcg	192
Ser	Glu	Asn	Arg	Thr	Asn	Leu	Ser	Cys	Glu	Gly	Cys	Leu	Ser	Pro	Ser	
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tgt	ctc	tcc	tta	ctt	cat	ctc	cag	gaa	aaa	aac	tgg	tct	gct	tta	ctg	240
Cys	Leu	Ser	Leu	Leu	His	Leu	Gln	Glu	Lys	Asn	Trp	Ser	Ala	Leu	Leu	
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Thr Ala Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile	
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Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe	
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Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met	
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Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg Trp Pro Leu Pro	
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Ser Lys Leu Cys Ala Val Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr	
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Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala	
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Ile Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala	
180 185 190	
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Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met	
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Pro Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu	
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Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe	
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Val Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu	
245 250 255	
act atc aag tca ctc cag aaa gaa gct act ttg tgt gta agt gat ctt	816
Thr Ile Lys Ser Leu Gln Lys Glu Ala Thr Leu Cys Val Ser Asp Leu	
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Gly Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser	
275 280 285	
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Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly	
290 295 300	
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Ser Tyr Thr Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys	
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Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp	
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Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser	
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Cys Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile	
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Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn	
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Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys	
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Leu Ala Tyr Lys Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser	
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Lys Gln Asp Ala Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu	
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Gly Lys Gln His Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val	
450 455 460	

aat gaa aag gtg agc tgt gtg tga tag gct agt tgc cgt ggc aac tgt 1440
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 35 40 45
 Ser Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys Leu Ser Pro Ser
 50 55 60
 Cys Leu Ser Leu Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu
 65 70 75 80
 Thr Ala Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile
 85 90 95
 Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe
 100 105 110
 Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met
 115 120 125
 Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg Trp Pro Leu Pro
 130 135 140
 Ser Lys Leu Cys Ala Val Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr
 145 150 155 160
 Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala
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 Ile Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala
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 Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met
 195 200 205
 Pro Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu
 210 215 220
 Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe
 225 230 235 240
 Val Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu
 245 250 255
 Thr Ile Lys Ser Leu Gln Lys Glu Ala Thr Leu Cys Val Ser Asp Leu
 260 265 270
 Gly Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser

275	280	285
Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly		
290	295	300
Ser Tyr Thr Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys		
305	310	315
Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp		
325	330	335
Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser		
340	345	350
Cys Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile		
355	360	365
Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn		
370	375	380
Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys		
385	390	395
Glu Asn Lys Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala		
405	410	415
Leu Ala Tyr Lys Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser		
420	425	430
Lys Gln Asp Ala Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu		
435	440	445
Gly Lys Gln His Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val		
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Asn Glu Lys Val Ser Cys Val		
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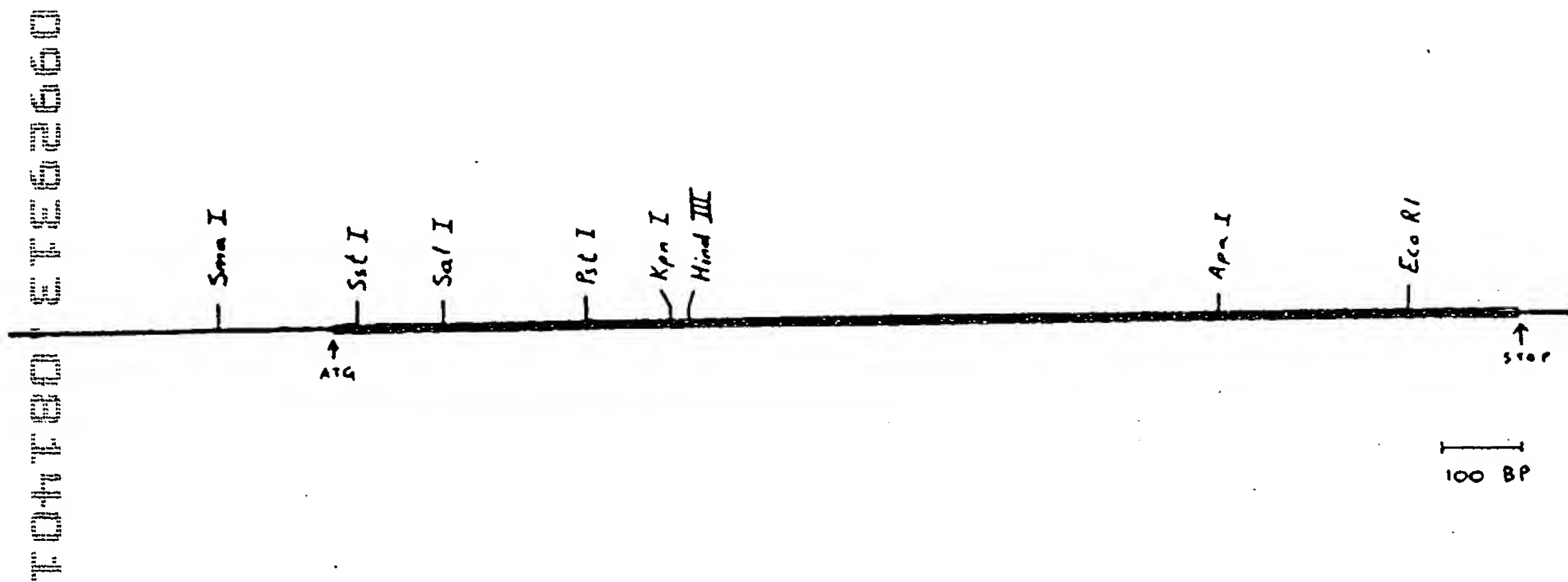
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Asn	Ser	Arg	Asp	Ala	Asn	Thr	Ser	Glu	Ala	Ser	Asn	Trp	Thr	Ile	Asp				
	35						40					45							
Ala	Glu	Asn	Arg	Thr	Asn	Leu	Ser	Cys	Glu	Gly	Tyr	Leu	Pro	Pro	Thr				
	50					55					60								
Cys	Leu	Ser	Ile	Leu	His	Leu	Gln	Glu	Lys	Asn	Trp	Ser	Ala	Leu	Leu				
	65				70					75					80				
Thr	Thr	Val	Val	Ile	Ile	Leu	Thr	Ile	Ala	Gly	Asn	Ile	Leu	Val	Ile				
				85					90					95					
Met	Ala	Val	Ser	Leu	Glu	Lys	Lys	Leu	Gln	Asn	Ala	Thr	Asn	Tyr	Phe				
			100					105					110						
Leu	Met	Ser	Leu	Ala	Ile	Ala	Asp	Met	Leu	Leu	Gly	Phe	Leu	Val	Met				
		115					120					125							
Pro	Val	Ser	Met	Leu	Thr	Ile	Leu	Tyr	Gly	Tyr	Arg	Trp	Pro	Leu	Pro				
	130					135					140								
Ser	Lys	Leu	Cys	Ala	Ile	Trp	Ile	Tyr	Leu	Asp	Val	Leu	Phe	Ser	Thr				
	145				150					155					160				
Ala	Ser	Ile	Met	His	Leu	Cys	Ala	Ile	Ser	Leu	Asp	Arg	Tyr	Val	Ala				
				165					170					175					
Ile	Gln	Asn	Pro	Ile	His	His	Ser	Arg	Phe	Asn	Ser	Arg	Thr	Lys	Ala				
			180					185					190						
Phe	Leu	Lys	Ile	Ile	Ala	Val	Trp	Thr	Ile	Ser	Val	Gly	Ile	Ser	Met				
		195					200					205							
Pro	Ile	Pro	Val	Phe	Gly	Leu	Gln	Asp	Asp	Ser	Lys	Val	Phe	Lys	Glu				
	210					215					220								
Gly	Ser	Cys	Leu	Leu	Ala	Asp	Asp	Asn	Phe	Val	Leu	Ile	Gly	Ser	Phe				
	225				230					235					240				
Val	Ala	Phe	Phe	Ile	Pro	Leu	Thr	Ile	Met	Val	Ile	Thr	Tyr	Phe	Leu				
				245					250					255					
Thr	Ile	Lys	Ser	Leu	Gln	Lys	Glu	Ala	Thr	Leu	Cys	Val	Ser	Asp	Leu				
			260				265						270						
Ser	Thr	Arg	Ala	Lys	Leu	Ala	Ser	Phe	Ser	Phe	Leu	Pro	Gln	Ser	Ser				

275		280		285
Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly				
290		295		300
Ser Tyr Ala Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys				
305		310		315 320
Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp				
		325		330 335
Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser				
		340		345 350
Cys Asn Glu Asn Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile				
		355		360 365
Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn				
		370 375		380
Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys				
385		390		395 400
Glu Asn Arg Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala				
		405		410 415
Leu Ala Tyr Lys Ser Ser Gln Leu Gln Val Gly Gln Lys Lys Asn Ser				
		420		425 430
Gln Glu Asp Ala Glu Gln Thr Val Asp Asp Cys Ser Met Val Thr Leu				
		435		440 445
Gly Lys Gln Gln Ser Glu Glu Asn Cys Thr Asp Asn Ile Glu Thr Val				
		450 455		460
Asn Glu Lys Val Ser Cys Val				
465		470		



2/10
FIGURE 2

Met Asp Ile Leu Cys Glu Glu Asn Thr Ser
A T G C A T A T T C T T T G T G A A G A A A A T A C T T C T
10 20 30

Leu Ser Ser Thr Thr Asn Ser Leu Met Gln
T T G A G C T C A A C T A C G A A C T C C C T A A T G C A A
40 50 60

Leu Asn Asp Asp Thr Arg Leu Tyr Ser Asn
T T A A A T G A T G A C A C C A G G C T C T A C A G T A A T
70 80 90

Asp Phe Asn Ser Gly Glu Ala Asn Thr Ser
G A C T T T A A C T C C G G A G A A G C T A A C A C T T C T
100 110 120

Asp Ala Phe Asn Trp Thr Val Asp Ser Glu
G A T G C A T T T A A C T G G A C A G T C G A C T C T G A A
130 140 150

Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys
A A T C G A A C C A A C C T T T C C T G T G A A G G G T G C
160 170 180

FIGURE 2, CON'D

Leu Ser Pro Ser Cys Leu Ser Leu Leu His
 C T C T C A C C G T C G T G T C T C T C C T T A C T T C A T
 190 200 210

Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu
 C T C C A G G A A A A A A C T G G T C T G C T T T A C T G
 220 230 240

Thr Ala Val Val Ile Ile Leu Thr Ile Ala
 A C A G C C G T A G T G A T T A T T C T A A C T A T T G C T
 250 260 270

Gly Asn Ile Leu Val Ile Met Ala Val Ser
 G G A A A C A T A C T C G T C A T C A T G G C A G T G T C C
 280 290 300

Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn
 C T A G A G A A A A A G C T G C A G A A T G C C A C C A A C
 310 320 330

Tyr Phe Leu Met Ser Leu Ala Ile Ala Asp
 T A T T T C C T G A T G T C A C T T G C C A T A G C T G A T
 340 350 360

Met Leu Leu Gly Phe Leu Val Met Pro Val
 A T G C T G C T G G G T T T C C T T G T C A T G C C C G T G
 370 380 390

Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg
 T C C A T G T T A A C C A T C C T G T A T G G G T A C C G G
 400 410 420

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FIGURE 2, CONT'D

Trp	Pro	Leu	Pro	Ser	Lys	Leu	Cys	Ala	Val																							
T	G	G	C	C	T	C	T	G	C	C	G	A	G	C	A	A	G	C	T	T	T	G	T	G	C	A	G	T	C			
										430											440											450

Trp	Ile	Tyr	Leu	Asp	Val	Leu	Phe	Ser	Thr																							
T	G	G	A	T	T	A	C	C	T	G	G	A	C	G	T	G	C	T	C	T	T	C	T	C	C	A	C	G				
										460											470											480

Ala	Ser	Ile	Met	His	Leu	Cys	Ala	Ile	Ser																							
G	C	C	T	C	C	A	T	C	A	T	G	C	A	C	C	T	C	T	G	C	G	C	C	A	T	C	T	C	G			
										490											500											510

Leu	Asp	Arg	Tyr	Val	Ala	Ile	Gln	Asn	Pro																							
C	T	G	G	A	C	C	G	C	T	A	C	G	T	C	G	C	C	A	T	C	C	A	G	A	A	T	C	C	C			
										520											530											540

Ile	His	His	Ser	Arg	Phe	Asn	Ser	Arg	Thr																							
A	T	C	C	A	C	C	A	C	A	G	C	C	G	C	T	T	C	A	A	C	T	C	C	A	G	A	A	C	T			
										550											560											570

Lys	Ala	Phe	Leu	Lys	Ile	Ile	Ala	Val	Trp																							
A	A	G	G	C	A	T	T	T	C	T	G	A	A	A	A	T	C	A	T	T	G	C	T	G	T	T	T	G	G			
										580											590											600

Thr	Ile	Ser	Val	Gly	Ile	Ser	Met	Pro	Ile																							
A	C	C	A	T	A	T	C	A	G	T	A	G	G	T	A	T	A	T	C	C	A	T	G	C	C	A	A	T	A			
										610											620											630

Pro	Val	Phe	Gly	Leu	Gln	Asp	Asp	Ser	Lys																							
C	C	A	G	T	C	T	T	T	G	G	G	C	T	A	C	A	G	G	A	C	G	A	T	T	C	G	A	A	G			
										640											650											660

FIGURE 2, CONT'D

Val Phe Lys Glu Gly Ser Cys Leu Leu Ala
 G T C T T T A A G G A G G G G A G T T G C T T A C T T G C C
 670 680 690

Asp Asp Asn Phe Val Leu Ile Gly Ser Phe
 G A T G A T A A C T T T G T C C T G A T C G G C T C T T T T
 700 710 720

Val Ser Phe Phe Ile Pro Leu Thr Ile Met
~~G T G T C A T T T T T C A T T C C C T T A A C C A T C A T G~~
 730 740 750

Val Ile Thr Tyr Phe Leu Thr Ile Lys Ser
 G T G A T C A C C T A C T T T C T A A C T A T C A A G T C A
 760 770 780

Leu Gln Lys Glu Ala Thr Leu Cys Val Ser
 C T C C A G A A A G A A G C T A C T T T G T G T G T A A G T
 790 800 810

Asp Leu Gly Thr Arg Ala Lys Leu Ala Ser
 G A T C T T G G C A C A C G G G C C A A A T T A G C T T C T
 820 830 840

Phe Ser Phe Leu Pro Gln Ser Ser Leu Ser
 T T C A G C T T C C T C C C T C A G A G T T C T T T G T C T
 850 860 870

Ser Glu Lys Leu Phe Gln Arg Ser Ile His
 T C A G A A A A G C T C T T C C A G C G G T C G A T C C A T
 880 890 900

FIGURE 2, CONT'D

Arg Glu Pro Gly Ser Tyr Thr Gly Arg Arg
 A G G G A G C C A G G G T C C T A C A C A G G C A G G A G G
 910 920 930

Thr Met Gln Ser Ile Ser Asn Glu Gln Lys
 A C T A T G C A G T C C A T C A G C A A T G A G C A A A A G
 940 950 960

Ala Cys Lys Val Leu Gly Ile Val Phe Phe
 G C A T G C A A G G T G C T G G G C A T C G T C T T C T T C
 970 980 990

Leu Phe Val Val Met Trp Cys Pro Phe Phe
 C T G T T T G T G G T G A T G T G G T G C C C T T T C T T C
 1000 1010 1020

Ile Thr Asn Ile Met Ala Val Ile Cys Lys
 A T C A C A A A C A T C A T G G C C G T C A T C T G C A A A
 1030 1040 1050

Glu Ser Cys Asn Glu Asp Val Ile Gly Ala
 G A G T C C T G C A A T G A G G A T G T C A T T G G G G C C
 1060 1070 1080

Leu Leu Asn Val Phe Val Trp Ile Gly Tyr
 C T G C T C A A T G T G T T T G T T T G G A T C G G T T A T
 1090 1100 1110

Leu Ser Ser Ala Val Asn Pro Leu Val Tyr
 C T C T C T T C A G C A G T C A A C C C A C T A G T C T A C
 1120 1130 1140

FIGURE 2, CONT'D

Thr	Leu	Phe	Asn	Lys	Thr	Tyr	Arg	Ser	Ala
A	C	A	C	T	G	T	T	C	A
A	C	A	A	C	A	A	G	A	C
C	T	A	T	A	G	G	T	C	A
G	C	C							
			1150			1160			1170

Phe	Ser	Arg	Tyr	Ile	Gln	Cys	Gln	Tyr	Lys
T	T	T	T	C	A	C	G	G	T
A	T	A	T	T	C	A	G	T	G
T	C	A	G	T	A	C	A	G	A
A	A	G							
			1180			1190			1200

Glu	Asn	Lys	Lys	Pro	Leu	Gln	Leu	Ile	Leu
G	A	A	A	C	A	A	A	A	A
A	A	A	A	A	A	A	A	A	A
C	C	A	T	T	G	C	A	G	T
T	A	A	T	T	T	A			
			1210			1220			1230

Val	Asn	Thr	Ile	Pro	Ala	Leu	Ala	Tyr	Lys
G	T	G	A	A	C	A	C	A	A
T	A	C	C	G	G	C	T	T	T
G	G	C	C	T	A	C	A	A	G
			1240			1250			1260

Ser	Ser	Gln	Leu	Gln	Met	Gly	Gln	Lys	Lys
T	C	T	A	G	C	C	A	A	C
T	T	C	A	A	A	T	G	G	G
A	C	A	A	A	A	A	A	A	A
A	A	A	A	A	A	A	A	A	A
			1270			1280			1290

Asn	Ser	Lys	Gln	Asp	Ala	Lys	Thr	Thr	Asp
A	A	T	T	C	A	A	A	G	C
A	A	G	C	A	A	G	A	T	G
C	C	A	A	G	A	C	A	A	C
A	G	A	T						
			1300			1310			1320

Asn	Asp	Cys	Ser	Met	Val	Ala	Leu	Gly	Lys
A	A	T	G	A	C	T	G	C	T
C	A	A	T	G	G	T	T	G	C
T	C	T	A	G	G	A	A	A	A
A	A	G							
			1330			1340			1350

Gln	His	Ser	Glu	Glu	Ala	Ser	Lys	Asp	Asn
C	A	G	C	A	T	T	C	T	G
A	A	G	A	G	A	G	G	C	T
T	C	T	A	A	A	G	A	C	A
A	A	T							
			1360			1370			1380

FIGURE 2, CONT'D

Ser Asp Gly Val Asn Glu Lys Val Ser Cys
A G C G A C G G A G T G A A T G A A A A G G T G A G C T G T
1390 1400 1410

Val *** Ala Ser Cys Arg Gly Asn Cys
G T G T G A T A G G C T A G T T G C C G T G G C A A C T G T
1420 1430 1440

G G A A G G C A C A C T G A G C A A G T T T T C A C C T A T
1450 1460 1470

C T G G T T T T T T T T G

1480

FIGURE 3

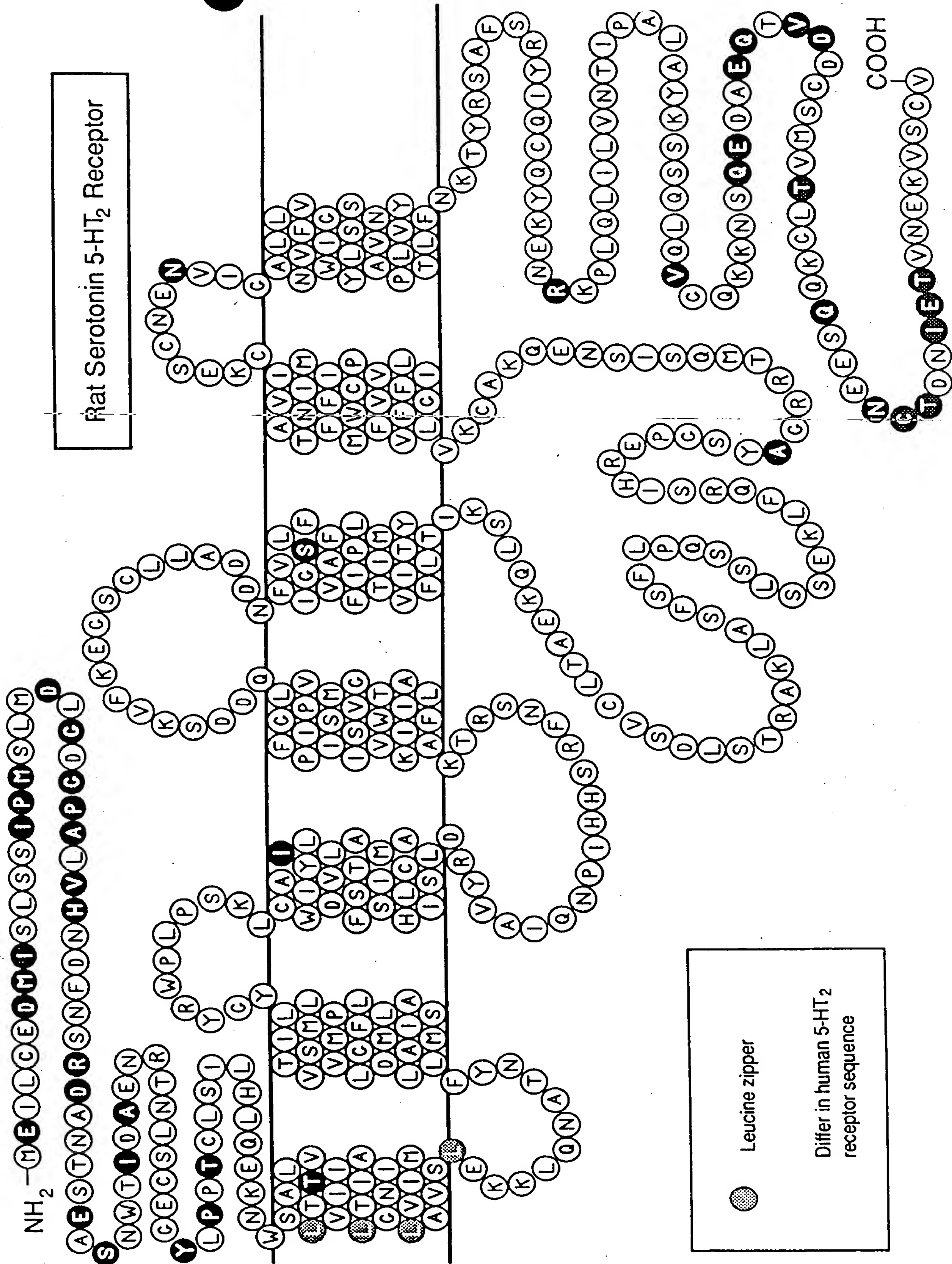


FIGURE 4

